plus sulfadiazine was started without clinical and radiological benefits. On the twelfth day a lumbar puncture was performed and the fluid result was normal. On the fifteenth day because of the development of pancytopenia a sternal puncture was made but no haematologic disorders or parasitic infections were diagnosed. An osteomedullary biopsy, on the contrary, revealed medullary leishmaniasis. The patient started the therapy with liposomal amphotericin B and he left the hospital after 10 days with resolution of fever and pancytopenia. Amphotericin B was continued with one infusion a week for 4 weeks.
Conclusion: In HIV positive patients, visceral leishmaniasis may be the first opportunistic manifestation of HIV infection, even if it is rare, or it may occur late in the course of the disease. Relapse of visceral leishmaniasis usually occurs within 6 months after treatment. Chronic suppressive therapy is probably advisable in persons with HIV, especially for subject with low CD4+ and high viral load, but the optimal drug and regimen have not yet been defined.

Microbial infections regulate expression of HIV-1 co-receptors

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Background: While immune suppression secondary to HIV-1 infection leads to opportunistic infections, microbial infections variably modulate replication of HIV-1 or HIV-1 disease progression. Chemokine receptors CCR5 and CXCR4 are essential for entry of HIV-1 into cell, and their expression is regulated by immunological stimulation. We studied expression of CCR5 or CXCR4 upon stimulation with a variety of microbial pathogens including Epstein-Barr virus (EBV), *Orientia tsutsugamushi*, or *Plasmodium falciparum*.
Methods: Peripheral blood mononuclear cells (PBMC) were isolated from healthy control individuals or patients with acute EBV infection. Where indicated, PBMC were stimulated with heat-inactivated *O. tsutsugamushi* or *P. falciparum*. Expression of CCR5 or CXCR4 is determined by flow cytometric analysis. Infectability of cells by R5 or X4 HIV-1 was determined by conventional infection assays as well as single round viral infection assays. Levels of proinflammatory cytokines or chemokines were determined by commercially available ELISA kits.
Results: Expression of CCR5, but not CXCR4, on CD4+ T cells derived from acutely EBV infected individuals was enhanced, resulting in increased infectability of cells by R5-HIV-1, but not by X4-HIV-1. In contrast, expression of CCR5 on CD4+ T cells exposed to *O. tsutsugamushi* or *P. falciparum* was markedly down-regulated, rendering these cells relatively resistant to R5-HIV-1 infection. However, when cells already infected with HIV-1 were stimulated with these microbial stimuli, HIV-1 expression was enhanced, at least in part by production of proinflammatory cytokines.
Conclusions: Effects of microbial infections on HIV-1 infection appear to be variable, depending on microbial pathogens, HIV-1 strains or time of microbial stimulation.

Genetic diversity of KSHV strains from AIDS-associated Kaposi's sarcoma in Brazil

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Background: Kaposi's sarcoma-associated herpesvirus (KSHV) or HHV 8 has been found in KS tumour tissue, regardless its clinical forms. In despite of the impact of the highly active antiretroviral therapy having reduced the AIDS-associated opportunistic infectious diseases, KS remains as the most common AIDS-associated neoplasia. Based on a hypervariable open region frame region (ORF K1), five KSHV subtypes have been described: A, from USA and Europe; B from Equatorial Africa; C from the Mediterranean and Middle East; D from The Pacific Islands and E from The Amazon region in Brazil.
Objectives: 1. To classify the strains of KSHV isolated from AIDS-associated KS in Brazil. 2. To construct a phylogenetic tree with the KSHV/DNA isolates obtained.
Patients and Methods: AIDS/KS patients were selected from a cross-sectional study to analyze HIV risk behaviour and the KSHV strains distribution carried out in Sao Paulo, Brazil. DNA was extracted from the KS tumour tissue by using the QIAgen commercial kit. KSHV/DNA fragments sized 460 bp of the ORF K1 loops regions, VR1 and VR2 were amplified by nested PCR. The DNA sequences were aligned by clustal and a phylogenetic tree was constructed by using the Neighbor-joining technique.
Results: 26 samples from 24 AIDS/KS patients were analyzed. The median CD4 count was 248. Most of Brazilian samples clustered into two subtypes: A and C. Subtype A was found in 12/26 (46.1%), B in 2/26 (7.7%) and C in 12/26 (46.1%) samples Two patients had samples collected from two different sites. The distribution of KSHV strains according to risk behaviour for HIV infection, showed that 7/11 (63.6%) patients with C subtype were heterosexual and 2/11 (18.2%) were homosexual. 4/11 (36.4) patients with A subtype were heterosexual and 5/11 (45.4%) were homosexual. One homosexual and another one heterosexual patients yielded subtype B. 4 patients had unknown risk behaviour
Conclusions: 1. Brazilian KSHV strains clustered mainly into subtypes A and C; 2.Most of heterosexual patients were infected by KSHV C strain.